

#6

Atty. Docket No: 16313-0037

In re patent application of

COSTA E SILVA, OSWALDO DA et al.

Serial No. 09/828,447

Filed: April 6, 2001

For: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
OF USE IN PLANTS

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

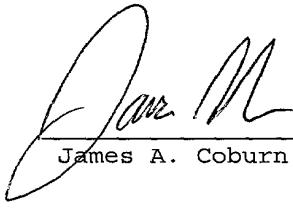
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,


Date

25,2001


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SEQUENCE LISTING

<110> COSTA E SILVA, OSWALDO DA
BOHNERT, HANS J.
VAN THIELEN, NOCHA
CHEN, ROUYING
ISHITANI, MANABU

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OF USE IN PLANTS

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<141> 2001-04-06

<150> 60/196,001

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 gcccgttgc tgcgtatgttgc gtttgc tgcgtatgttgc ggtatgtatc aaggcatttca aggaaatggc 1140
 gtttgc tgcgtatgttgc gtttgc tgcgtatgttgc ggtatgtatc aaggcatttca aggaaatggc 1200
 cccagatgttgc tgcgtatgttgc gtttgc tgcgtatgttgc ggtatgtatc aaggcatttca aggaaatggc 1260
 gacaattttca ttttgc tgcgtatgttgc gtttgc tgcgtatgttgc ggtatgtatc aaggcatttca aggaaatggc 1320
 aaagctacttgc gtttgc tgcgtatgttgc gtttgc tgcgtatgttgc ggtatgtatc aaggcatttca aggaaatggc 1380

aaacttcaag cggatcaata tagctcacag aatccattct tcgtttctgt ttcctgagaa 1440
 cccaccaatg tccaaagtac aaaaactccgt gggagaaaca gacgtgcagt gcatgcataa 1500
 gttgggtgtg attgtttgcg tagtgatgtt tctgatgac ttgaatagaa tcaagtgcac 1560
 agatagtcacaa ttgtctcaca caagatctc gaacaatcca ccaaccggcg ttgccagtcg 1620
 tgccggagggc acgggtggc ggacggacta gccgtgcac gcgttagag aatgcattgg 1680
 cggctgcaga ttagacagtt gttcgatcc gttgttagat agatcgtag gatactcgac 1740
 tcttacctgt gttcaattc cggcatcgga agcccccgag tgaaaattgg acgagctcg 1800

<210> 11
 <211> 1054
 <212> PRT
 <213> Physcomitrella patens

<400> 11
 Met Cys Ser Ile Pro Phe Gly Arg Lys Lys Ser Lys Lys Gly Asp Leu
 1 5 10 15
 Ala Gln Asp Leu Leu Gly Asp Val Phe Ser Thr Tyr Ser Glu Asn Gly
 20 25 30
 Lys Leu Asp Ala Glu Gly Leu Leu Lys Phe Leu Gln Thr Glu Gln Gly
 35 40 45
 Asp Ser Lys Ser Ser Leu Asp Asp Ala Lys His Leu Val Glu Leu Ile
 50 55 60
 Arg Asn Glu Arg His Lys Ser Lys Phe Pro Gly Phe Ile Val Ser Ser
 65 70 75 80
 Asp Leu Ser Lys Gly Asp Phe Lys Asn Tyr Val Leu Ser Pro Asp Leu
 85 90 95
 Asn Gly Val Leu Glu Ser Thr Val His Gln Asp Met Thr Gln Pro Leu
 100 105 110
 Ser His Tyr Phe Ile Phe Thr Gly His Asn Ser Tyr Leu Thr Gly Asn
 115 120 125
 Gln Leu Ser Ser Asp Ser Ser Asp Val Pro Ile Ala Ala Ala Leu Gln
 130 135 140
 Arg Gly Val Arg Val Val Glu Leu Asp Leu Trp Pro Asp Asp Lys Gly
 145 150 155 160
 Gly Ile Lys Val Thr His Gly Asn Thr Leu Thr Ser Pro Val Ala Phe
 165 170 175
 Glu Lys Cys Ile Lys Ala Ile Lys Ala Asn Ala Phe Val Ser Ser Lys
 180 185 190
 Tyr Pro Val Val Ile Thr Leu Glu Asp His Leu Ser Ser Pro Leu Gln
 195 200 205
 Ala Leu Ala Ala Glu Thr Leu Thr Asn Ile Leu Gly Glu Asp Leu Tyr
 210 215 220

Tyr Pro Pro Ser Ser Asp Gly Phe Lys Glu Leu Pro Ser Pro Glu Ser
 225 230 235 240
 Leu Lys Gly Lys Ile Leu Ile Ser Thr Lys Pro Pro Lys Glu Tyr Leu
 245 250 255
 Glu Ala Ala Val Ala Gln Lys Ser Ala Leu Lys Asp Glu Lys Ile Leu
 260 265 270
 Asn Glu Phe Lys Lys Ala Asp Lys Leu Gln Glu Gln Ser Thr Ala Pro
 275 280 285
 Val Lys Ser Pro Val Glu Lys Lys Ile Ala Val Pro Pro Ser Glu Lys
 290 295 300
 Thr Lys Ser Ile Ser Glu Glu Lys Asp Leu Ser Glu Lys Val Gly Asn
 305 310 315 320
 Leu Arg Val Asp Ser Glu Gly Glu Ser Ala Asp Pro Ala Pro Ala Ser
 325 330 335
 Ser Pro Asp Gly Lys Lys Ala Thr Leu Thr Ala Asp Ser Glu Ser Asp
 340 345 350
 Asp Asp Asp Asn Lys Lys Asn Pro Glu Tyr Ala Arg Leu Ile Thr Ile
 355 360 365
 His Gln Ser Lys Pro Ser Lys Gly Thr Thr Val Glu Asp Arg Leu Lys
 370 375 380
 Val Glu Gly Thr Val Val Arg Ile Ser Leu Ser Glu Thr Lys Leu Glu
 385 390 395 400
 Lys Val Thr Glu Glu Phe Pro Glu Leu Val Val Lys Phe Thr Gln Arg
 405 410 415
 Asn Ile Leu Arg Met Cys Ser Ile Pro Phe Gly Arg Lys Lys Ser Lys
 420 425 430
 Lys Gly Asp Leu Ala Gln Asp Leu Leu Gly Asp Val Phe Ser Thr Tyr
 435 440 445
 Ser Glu Asn Gly Lys Leu Asp Ala Glu Gly Leu Leu Lys Phe Leu Gln
 450 455 460
 Thr Glu Gln Gly Asp Ser Lys Ser Ser Leu Asp Asp Ala Lys His Leu
 465 470 475 480
 Val Glu Leu Ile Arg Asn Glu Arg His Lys Ser Lys Phe Pro Gly Phe
 485 490 495
 Ile Val Ser Ser Asp Leu Ser Lys Gly Asp Phe Lys Asn Tyr Val Leu
 500 505 510
 Ser Pro Asp Leu Asn Gly Val Leu Glu Ser Thr Val His Gln Asp Met
 515 520 525

Thr Gln Pro Leu Ser His Tyr Phe Ile Phe Thr Gly His Asn Ser Tyr
 530 535 540
 Leu Thr Gly Asn Gln Leu Ser Ser Asp Ser Ser Asp Val Pro Ile Ala
 545 550 555 560
 Ala Ala Leu Gln Arg Gly Val Arg Val Val Glu Leu Asp Leu Trp Pro
 565 570 575
 Asp Asp Lys Gly Gly Ile Lys Val Thr His Gly Asn Thr Leu Thr Ser
 580 585 590
 Pro Val Ala Phe Glu Lys Cys Ile Lys Ala Ile Lys Ala Asn Ala Phe
 595 600 605
 Val Ser Ser Lys Tyr Pro Val Val Ile Thr Leu Glu Asp His Leu Ser
 610 615 620
 Ser Pro Leu Gln Ala Leu Ala Ala Glu Thr Leu Thr Asn Ile Leu Gly
 625 630 635 640
 Glu Asp Leu Tyr Tyr Pro Pro Ser Ser Asp Gly Phe Lys Glu Leu Pro
 645 650 655
 Ser Pro Glu Ser Leu Lys Gly Lys Ile Leu Ile Ser Thr Lys Pro Pro
 660 665 670
 Lys Glu Tyr Leu Glu Ala Ala Val Ala Gln Lys Ser Ala Leu Lys Asp
 675 680 685
 Glu Lys Ile Leu Asn Glu Phe Lys Lys Ala Asp Lys Leu Gln Glu Gln
 690 695 700
 Ser Thr Ala Pro Val Lys Ser Pro Val Glu Lys Lys Ile Ala Val Pro
 705 710 715 720
 Pro Ser Glu Lys Thr Lys Ser Ile Ser Glu Glu Lys Asp Leu Ser Glu
 725 730 735
 Lys Val Gly Asn Leu Arg Val Asp Ser Glu Gly Glu Ser Ala Asp Pro
 740 745 750
 Ala Pro Ala Ser Ser Pro Asp Gly Lys Lys Ala Thr Leu Thr Ala Asp
 755 760 765
 Ser Glu Ser Asp Asp Asp Asp Asn Lys Lys Asn Pro Glu Tyr Ala Arg
 770 775 780
 Leu Ile Thr Ile His Gln Ser Lys Pro Ser Lys Gly Thr Thr Val Glu
 785 790 795 800
 Asp Arg Leu Lys Val Glu Gly Thr Val Val Arg Ile Ser Leu Ser Glu
 805 810 815
 Thr Lys Leu Glu Lys Val Thr Glu Glu Phe Pro Glu Leu Val Val Lys
 820 825 830

Phe Thr Gln Arg Asn Ile Leu Arg Val Tyr Pro Ala Gly Asn Arg Val
 835 840 845
 Asn Ser Ser Asn Tyr Asp Pro Thr Ala Ala Trp Ile His Gly Ala Gln
 850 855 860
 Met Val Ala Gln Asn Met Gln Gly Tyr Gly Lys Glu Leu Trp Gln Ala
 865 870 875 880
 His Gly Lys Phe Arg Gly Asn Gly Gly Cys Gly Tyr Ile Leu Lys Pro
 885 890 895
 Lys Tyr Leu Leu Glu Asp Leu Pro Asn Gly Lys Pro Phe Asn Pro Ser
 900 905 910
 Ala Pro Gly Asp Thr Lys Met Ile Leu Lys Val Lys Val Met Thr Thr
 915 920 925
 Met Gly Trp Asp Lys Ala Phe Pro Lys Tyr His Phe Asp Leu Phe Ser
 930 935 940
 Pro Pro Asp Phe Phe Thr Arg Leu Leu Val Thr Gly Val Pro Ala Asp
 945 950 955 960
 Val Ala Lys Trp Lys Thr Ser Val Ile Asp Asp Val Trp Glu Pro His
 965 970 975
 Trp Asn Glu Asp His Glu Phe Tyr Leu Lys Cys Pro Glu Leu Ala Leu
 980 985 990
 Leu Arg Ile Glu Val Arg Asp His Asp Glu Glu Ser Gln Asp Glu Phe
 995 1000 1005
 Glu Gly Gln Ala Cys Leu Pro Met His Glu Ile Lys Asp Gly Tyr Arg
 1010 1015 1020
 Cys Val Gln Met Tyr Asp Lys Lys Gly Ser Val Leu Lys Gly Val Lys
 1025 1030 1035 1040
 Met Leu Phe His Phe Gln Lys Arg Ser Phe Ser Pro Val Gln
 1045 1050

<210> 12
 <211> 628
 <212> PRT
 <213> *Physcomitrella patens*

<400> 12
 Met Cys Ser Ile Ala Cys Cys Arg Ser Gly Thr Pro Lys Gly Asp Pro
 1 5 10 15
 Glu Gln Asp Leu Val Gly Glu Val Phe Thr Ile Tyr Ser Glu Asn Glu
 20 25 30
 Arg Met Ser Ala Glu Gly Leu Leu Lys Phe Leu His Thr Glu Gln Gly
 35 40 45

Asp	Val	Asp	Phe	Thr	Leu	Asp	Asp	Ala	Lys	Gln	Ile	Met	Glu	Arg	Ile
50						55						60			
Arg	Lys	Asp	Trp	Lys	Lys	Ser	Phe	Gly	Leu	Ala	Ser	Ile	Asn	Ser	Asp
65					70						75			80	
Leu	Ser	Lys	Glu	Ala	Phe	Arg	Lys	Tyr	Leu	Met	Asn	Pro	Asp	Leu	Asn
					85					90				95	
Gly	Val	Leu	His	Asn	Val	Val	His	Gln	Asp	Met	Thr	Gln	Pro	Met	Ser
					100				105				110		
His	Tyr	Phe	Ile	Phe	Thr	Gly	His	Asn	Ser	Tyr	Leu	Thr	Gly	Asn	Gln
					115				120				125		
Leu	Ser	Ser	Asp	Ser	Ser	Asp	Thr	Pro	Ile	Ala	Ala	Leu	Arg	Arg	
					130				135				140		
Gly	Val	Arg	Val	Val	Glu	Leu	Asp	Leu	Trp	Pro	Asp	Asp	Lys	Gly	Gly
					145				150			155			160
Met	Lys	Val	Thr	His	Gly	Asn	Thr	Leu	Thr	Asn	Pro	Val	Ser	Phe	Gln
					165				170				175		
Lys	Cys	Val	Thr	Ala	Ile	Lys	Asn	Asn	Ala	Phe	Phe	Thr	Ser	Glu	Tyr
					180				185				190		
Pro	Val	Cys	Val	Thr	Ile	Glu	Asp	His	Leu	Thr	Ser	Glu	Leu	Gln	Gly
					195				200				205		
His	Ala	Ala	Glu	Ile	Leu	Glu	Gln	Ile	Leu	Gly	Asp	Ala	Leu	Tyr	Tyr
					210				215				220		
Pro	Pro	Thr	Thr	Asp	Ala	Leu	Val	Glu	Phe	Pro	Ser	Pro	Glu	Ser	Leu
					225				230			235			240
Lys	Arg	Lys	Ile	Ile	Ile	Ser	Thr	Lys	Pro	Pro	Lys	Glu	Tyr	Leu	Glu
					245				250				255		
Ala	Cys	Ser	Thr	Gln	Lys	Leu	Ala	Met	Glu	Asn	Arg	Asn	Leu	Val	Glu
					260				265				270		
Glu	Leu	Glu	Lys	Glu	Asp	Lys	Leu	Glu	Gln	Thr	Thr	Phe	Ala	Pro	Leu
					275				280				285		
Glu	Glu	Asn	His	Ile	Leu	Gly	Glu	Asn	Thr	Pro	Ser	Leu	Arg	Lys	Glu
					290				295				300		
Val	Glu	Val	Leu	Ser	Gln	Lys	Glu	Met	Ser	Thr	Pro	Ala	Glu	Leu	Asn
					305				310			315			320
Ser	Arg	Ser	Pro	Ser	Asp	Leu	Gly	Glu	Ala	Thr	Ser	Thr	Arg	Tyr	Ser
					325				330				335		
Lys	Ser	Asn	Asp	Gly	Asn	Asp	Asn	Pro	Lys	His	Phe	Lys	Tyr	Ala	Arg
					340				345				350		

Leu Ile Thr Ile Arg Leu Ala Lys His Ala Lys Gly Thr Ser Met Glu
 355 360 365

His Arg Leu Gln Val Asp Glu Ser Val Lys Arg Ile Ser Leu Ser Glu
 370 375 380

Ser Lys Leu Glu Lys Val Val Glu Lys Trp Pro Glu Ala Leu Val Lys
 385 390 395 400

Phe Thr Gln Lys Asn Ile Leu Arg Val Tyr Pro Ala Ala Asn Arg Val
 405 410 415

Asn Ser Ser Asn Phe Cys Pro Thr Leu Ala Trp Asn Tyr Gly Ala Gln
 420 425 430

Met Val Ala Gln Asn Met Gln Gly Tyr Gly Lys Glu Leu Trp Gln Ala
 435 440 445

Phe Gly Lys Phe Lys Gly Asn Gly Gly Cys Gly Tyr Val Leu Lys Pro
 450 455 460

Gln Tyr Leu Leu Glu Asn Leu Pro Ser Gly Val Pro Phe Asn Pro Thr
 465 470 475 480

Ser Pro Arg Asn Thr Thr Leu Ile Leu Lys Ile Lys Val Met Thr Thr
 485 490 495

Leu Gly Trp Asp Lys Ala Phe Ser Lys Arg His Phe Asp Leu Phe Ser
 500 505 510

Pro Pro Asp Phe Phe Thr Arg Val Ile Val Val Gly Val Pro Ala Asp
 515 520 525

Glu Ala Lys Trp Lys Thr Ser Val Val Asp Asn Ser Trp Ala Pro His
 530 535 540

Trp Asn Glu Asp His Glu Phe Ala Leu Lys Cys Pro Glu Leu Ala Leu
 545 550 555 560

Leu Arg Ile Glu Val Arg Asp His Asp Asp Asp Ser Lys Asp Glu Phe
 565 570 575

Glu Gly Gln Thr Cys Leu Pro Ile His Glu Val Arg Asp Gly Tyr Arg
 580 585 590

Cys Met Gln Met Tyr Asp Lys Lys Gly Asn Val Leu Lys Gly Val Leu
 595 600 605

Met Leu Phe His Phe Gln Lys Cys Lys Cys Thr Phe Gln Asp Thr Ala
 610 615 620

Pro Ile Ser Ser
 625

<210> 13
 <211> 258
 <212> PRT

<213> Physcomitrella patens

<400> 13

Met	Ser	Thr	Glu	Lys	Glu	Arg	Glu	Ser	Tyr	Val	Tyr	Met	Ala	Lys	Leu
1				5					10			15			
Ala	Glu	Gln	Ala	Glu	Arg	Tyr	Asp	Glu	Met	Val	Glu	Ser	Met	Lys	Lys
	20				25						30				
Val	Ala	Lys	Leu	Asp	Val	Glu	Leu	Thr	Val	Glu	Glu	Arg	Asn	Leu	Leu
		35				40						45			
Ser	Val	Gly	Tyr	Lys	Asn	Val	Ile	Gly	Ala	Arg	Arg	Ala	Ser	Trp	Arg
	50				55					60					
Ile	Met	Ser	Ser	Ile	Glu	Gln	Lys	Glu	Glu	Ser	Lys	Gly	Asn	Glu	Gln
	65				70					75			80		
Asn	Val	Lys	Arg	Ile	Lys	Asp	Tyr	Arg	His	Lys	Val	Glu	Glu	Glu	Leu
		85				90						95			
Ser	Lys	Ile	Cys	Asn	Asp	Ile	Leu	Ser	Ile	Ile	Asp	Gly	His	Leu	Ile
	100					105						110			
Pro	Ser	Ser	Ser	Thr	Gly	Glu	Ser	Thr	Val	Phe	Tyr	Tyr	Lys	Met	Lys
	115					120						125			
Gly	Asp	Tyr	Tyr	Arg	Tyr	Leu	Ala	Glu	Phe	Lys	Thr	Gly	Asn	Glu	Arg
	130					135						140			
Lys	Glu	Ala	Ala	Asp	Gln	Ser	Leu	Lys	Ala	Tyr	Gln	Ala	Ala	Ser	Ser
	145					150				155			160		
Thr	Ala	Val	Thr	Asp	Leu	Ala	Pro	Thr	His	Pro	Ile	Arg	Leu	Gly	Leu
		165				170						175			
Ala	Leu	Asn	Phe	Ser	Val	Phe	Tyr	Tyr	Glu	Ile	Leu	Asn	Ser	Pro	Glu
		180				185						190			
Arg	Ala	Cys	His	Leu	Ala	Lys	Gln	Ala	Phe	Asp	Glu	Ala	Ile	Ala	Glu
	195					200						205			
Leu	Asp	Thr	Leu	Ser	Glu	Glu	Ser	Tyr	Lys	Asp	Ser	Thr	Leu	Ile	Met
	210				215						220				
Gln	Leu	Leu	Arg	Asp	Asn	Leu	Thr	Leu	Trp	Thr	Ser	Asp	Leu	Gln	Asp
	225					230			235					240	
Glu	Gly	Gly	Asp	Asp	Gln	Gly	Lys	Gly	Asp	Asp	Met	Arg	Pro	Glu	Glu
		245				250						255			
Ala	Glu														

<210> 14

<211> 257

<212> PRT

<213> Physcomitrella patens

<400> 14
 Met Thr Glu Leu Arg Glu Glu Asn Val Tyr Met Ala Lys Leu Ala Glu
 1 5 10 15

Gln Ala Glu Arg Tyr Asp Glu Met Val Glu Ala Met Glu Asn Val Val
 20 25 30

Lys Ala Val Glu Asn Glu Glu Leu Thr Val Glu Glu Arg Asn Leu Leu
 35 40 45

Ser Val Ala Phe Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg
 50 55 60

Ile Ile Ser Ser Ile Glu Gln Lys Glu Glu Ala Lys Gly Ser Glu Glu
 65 70 75 80

His Val Ala Ala Ile Lys Glu Tyr Arg Ser Lys Val Glu Ala Glu Leu
 85 90 95

Ser Thr Ile Cys Asp Thr Ile Leu Lys Leu Leu Asp Ser His Leu Ile
 100 105 110

Pro Ser Ser Thr Ser Gly Glu Ser Lys Val Phe Tyr Leu Lys Met Lys
 115 120 125

Gly Asp Tyr His Arg Tyr Leu Ala Glu Phe Lys Ala Gly Ala Glu Arg
 130 135 140

Lys Glu Ala Ala Glu Ala Thr Leu His Ala Tyr Lys His Ala Gln Asp
 145 150 155 160

Ile Ser Thr Thr Glu Leu Ala Ser Thr His Pro Ile Arg Leu Gly Leu
 165 170 175

Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Val Ser Pro Asp
 180 185 190

Arg Ala Cys His Leu Ala Lys Gln Ala Phe Asp Glu Ala Ile Ser Glu
 195 200 205

Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met
 210 215 220

Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Asp
 225 230 235 240

Asp Ile Gly Glu Glu Gly Lys Asp Ser Lys Val Glu Asp Ala Asp Asp
 245 250 255

His

<210> 15
 <211> 337
 <212> PRT
 <213> Physcomitrella patens

<400> 15
 Met Ser Thr Glu Gly Gly Leu His Val Leu Asp Gly Ser Gln Ile Arg
 1 5 10 15
 Asn Ala Leu Pro Asp Leu Gln Ser Arg Asn Ser Phe Ser Lys Asn Asp
 20 25 30
 Glu Gly Ser Lys Gly Tyr Leu Thr Pro Ser Glu Met Arg Gln Ala Ala
 35 40 45
 Glu Ala Glu Ala Ala Leu Leu Leu Gly Val Gln Leu Ser Ser Lys
 50 55 60
 Ile Phe Glu Asn Ala Ala Ser Lys Leu Pro Thr Glu Asp Ser Ala Glu
 65 70 75 80
 Ile Thr Glu Asp Val Phe Ser Ser Thr Leu Gln Ser Tyr Leu Thr Ala
 85 90 95
 Ile Ala Asp Ala Leu Glu Asp Glu Pro Val Val Val Ser Val Leu Asp
 100 105 110
 Gly Ser Ala Ile Lys Ala Leu Leu Glu Asp Glu Asp Phe Ala Met
 115 120 125
 Val Ala Glu Asp Leu Phe Glu Lys Leu Asp Thr Asp Glu Ser Gly Lys
 130 135 140
 Leu Ser Ser Lys Glu Leu Arg Pro Ala Ile Met Gln Leu Gly Val Glu
 145 150 155 160
 Gln Gly Val Pro Pro Ala Ala Ala Thr Thr Glu Ala Glu Glu Leu Val
 165 170 175
 Thr Lys Leu Ile Asn Lys Tyr Gly Gln Gly Thr Glu Glu Leu Gly Gln
 180 185 190
 Ala Gln Phe Ala Ala Leu Leu Gln Asp Val Leu Gln Asp Met Ala Glu
 195 200 205
 Ser Leu Ala Glu Lys Pro Ile Thr Ile Val Arg Asp Val Lys Met Leu
 210 215 220
 Asn Gly Ser His Leu Arg Lys Met Leu Ala Asp Glu Lys Ala Phe Lys
 225 230 235 240
 Glu Met Ala Asp Asn Met Phe Asn Asp Leu Asp Val Asn Lys Asp Gln
 245 250 255
 Arg Leu Ser Lys Ala Glu Ile Arg Pro Leu Phe Glu Gln Gln Thr Ala
 260 265 270
 Ala Trp Gly Leu Pro Pro Val Gly Asp Ser Asp Thr Glu Glu Leu Phe
 275 280 285
 Asp Glu Val Phe Lys Ala Val Asp Ser Asp Lys Ser Gly Glu Val Glu
 290 295 300

Lys Pro Glu Phe Ala Val Leu Val Lys Thr Leu Leu Ala Asp Phe Ala
 305 310 315 320

Glu Thr Leu Arg Leu Asn Pro Ile Leu Val Glu Ile Glu Thr Ala Ser
 325 330 335

Arg

<210> 16
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 16
 caggaaacag ctatgacc 18

<210> 17
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 17
 ctaaaggaa caaaagctg 19

<210> 18
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 18
 tgtaaaacga cggccagt 18

<210> 19
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 19
 caggtccgag ctgacgatga acccag 26

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<210> 20
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
atcccgggca atcgtcgggt gacattcctg ttc 33

<210> 21
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
gcgttaacca acacacctcagc gttccacatg cat 33

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
cgagctcctc caccagattc ctgttc 26

<210> 23
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
atcccgggct tcgggagttt aagaggatgt cacg 34

<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
gcgttaacct tgggtgcaca cactaaactg gtc 33

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<210> 25
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
atcccgccgcg gactgtcgtg gacgagtggtg ctag 34

<210> 26
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gcgagctcgg cacgcaactg cacatcttct tgc 33

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
accaggcctca acttagtcgc ctggac 26

<210> 28
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
gcgttaactt cacaatgacg gagctacgag agga 34

<210> 29
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29		
gcgagctcca gcctcaactt agtcgcctgg aca		33
<210> 30		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Primer		
<400> 30		
ccctgctcaa cgcccaagctg cataat		26
<210> 31		
<211> 32		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Primer		
<400> 31		
atccccgggtc agtcgtgga agtgttgcag ca		32
<210> 32		
<211> 33		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Primer		
<400> 32		
gcgagctcgt ccaattttca ctcggggct tcc		33
<210> 33		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Primer		
<400> 33		
gcgctgcaga tttcatttgg agaggacacg		30
<210> 34		
<211> 35		
<212> DNA		
<213> Artificial Sequence		

<220>		
<223> Description of Artificial Sequence: Primer		
<400> 34		
cgcgccggc ctcagaagaa ctcgtcaaga aggcg		35
<210> 35		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Primer		
<400> 35		
gctgacacgc caaggctcgc tagtc		25
<210> 36		
<211> 27		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Primer		
<400> 36		
ccagcttagc agcgacagta gcgacgt		27
<210> 37		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Primer		
<400> 37		
cagtctgtct tccacggtag ttcct		25
<210> 38		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Primer		
<400> 38		
ggccatggag aacaggaatc tgggtgg		26
<210> 39		
<211> 25		
<212> DNA		

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
gctccgtagt tccaaaggccag agtag 25

<210> 40
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40
gacactgatg agagtgccaa gctgag 26

<210> 41
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
gactcgatgc ttcaacgaga ggcag 25